

Orachorn Chotiyarnwong 2009: Phenotypic and Genetic Relationship in Indigenous and Recommended Thai Soybean Varieties. Master of Science (Agricultural Biotechnology), Major Field: Agricultural Biotechnology, Interdisciplinary Graduate Program. Thesis Advisor: Professor Peerasak Srinives, Ph.D. 240 pages.

Soybean is an important source of protein and oil. Information on genetic diversity and relationship among breeding materials is essential to a soybean breeder for efficient improvement of the crop. The objective of this study is to evaluate the genetic diversity and to group 160 Thai soybean varieties (149 indigenous and 11 recommended) using 26 morphological characters (11 quantitative and 15 qualitative) and 18 SSR markers. The experiments were conducted in 2 locations and 2 seasons. Clustering of 11 quantitative traits based on Euclidean distance and grouped by UPGMA revealed that the data obtained from the trial conducted at Kasetsart University, Kamphaeng Saen Campus (KU-KPS) in the dry season 2004/05, divided the soybean varieties into 22 groups at 34.56 % different level. The data from the trial conducted in the same season in Chiang Mai Field Crop Research Center (CMFCRC) separated them into 22 groups at 34.56 % different level. In rainy season 2005, the data from KU-KPS divided the soybean varieties into 22 groups at 26.88 % different level, while the data from CMFCRC separated them into 23 groups at 17.72 % different level. Environmental factors also affected quantitative traits such as days to flowering, days to harvest and plant height. So the soybean varieties were grouped in each environment. When data from 15 qualitative traits were used to evaluate similarity using simple matching and to group by UPGMA, the soybean varieties were separated into 23 groups at 80 % similarity level with $r = 0.60$. The qualitative characters, although not affected by environment, the polymorphism found in each character was rather limited. When 18 SSR markers were applied, they produced an average of 11.83 alleles. Satt458 gave the highest number of allele (22) and Satt045 gave the lowest number of allele (6). The SSR loci produced a mean gene diversity (H) of 0.831 with Satt458 gave the highest H value of 0.916, while Satt045 gave the lowest H value of 0.695. Clustering the Euclidean distance of allele size using the UPGMA method separated this population into 14 groups at 53.32 % different levels with $r = 0.91$. Used of molecular marker gave more powerful in grouped and identified the soybean varieties, we found that some of varieties may be the same one. This indicated that the indigenous and recommended soybean varieties in Thailand have high genetic diversity based on morphological and SSR markers. Although, the SSR markers seem to be reliable more than morphological characters in grouping soybean germplasm, morphological characters are indispensable for the plant breeders to classify and select suitable parents for soybean crosses.

Student's signature

Thesis Advisor's signature